OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/001,227

DATE: 12/10/2001
TIME: 15:00:38

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\12102001\I001227.raw

ENTERED

```
      4 <110> APPLICANT: KAPELLER-LIBERMANN
      5       SILOS-SANTIAGO
      7 <120> TITLE OF INVENTION: METHODS OF USING 18903 TO TREAT PAIN AND
      8       PAIN-RELATED DISORDERS
     10 <130> FILE REFERENCE: MNI-199
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/001,227
C--> 12 <141> CURRENT FILING DATE: 2001-11-30
     12 <150> PRIOR APPLICATION NUMBER: 60/250929
     13 <151> PRIOR FILING DATE: 2000-11-30
     15 <160> NUMBER OF SEQ ID NOS: 7
     17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
     19 <210> SEQ ID NO: 1
     20 <211> LENGTH: 1983
     21 <212> TYPE: DNA
     22 <213> ORGANISM: Homo sapiens
     24 <220> FEATURE:
     25 <221> NAME/KEY: CDS
     26 <222> LOCATION: (98)...(1849)
     28 <400> SEQUENCE: 1
     29 cctttagcca attcggccga ggcctcccgc cccagtactt gctggcaggg attaagagca 60
     30 gataaaagtg tgctcacaca ctgtagacac ggctacc atg cca tcc aca gtg ttg  115
     31                                         Met Pro Ser Thr Val Leu
     32                                          1               5
     34 cca tcc aca gtg ttg cca tca ctc ctg ccc aca gca gga gct ggc tgg   163
     35 Pro Ser Thr Val Leu Pro Ser Leu Leu Pro Thr Ala Gly Ala Gly Trp
     36              10                  15                  20
     38 agc atg agg tgg att ctg tgc tgg agc ctc acc ctc tgc ctg atg gcg   211
     39 Ser Met Arg Trp Ile Leu Cys Trp Ser Leu Thr Leu Cys Leu Met Ala
     40          25                  30                  35
     42 cag acg gcc ttg ggt gcc ttg cac acc aag agg cct caa gtg gtc acc   259
     43 Gln Thr Ala Leu Gly Ala Leu His Thr Lys Arg Pro Gln Val Val Thr
     44      40                  45                  50
     46 aaa tat gga acc ctg caa gga aaa cag atg cat gtg ggg aag aca ccc   307
     47 Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met His Val Gly Lys Thr Pro
     48  55                  60                  65                  70
     50 atc caa gtc ttt tta gga gtc ccc ttc tcc aga cct cct cta ggt atc   355
     51 Ile Gln Val Phe Leu Gly Val Pro Phe Ser Arg Pro Pro Leu Gly Ile
     52                  75                  80                  85
     54 ctc agg ttt gca cct cca gaa ccc ccg gag ccc tgg aaa gga atc aga   403
     55 Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu Pro Trp Lys Gly Ile Arg
     56              90                  95                  100
     58 gat gct acc acc tac ccg cct ggg tgc ctg cag gag tcc tgg ggc cag   451
     59 Asp Ala Thr Thr Tyr Pro Pro Gly Cys Leu Gln Glu Ser Trp Gly Gln
     60          105                 110                 115
     62 ctg gcc tcg atg tac gtc agc acg cgg gaa cgg tac aag tgg ctg cgc   499
     63 Leu Ala Ser Met Tyr Val Ser Thr Arg Glu Arg Tyr Lys Trp Leu Arg
     64      120                 125                 130
```

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 66 ttc agc gag gac tgt ctg tac ctg aac gtg tac gcg ccg gcg cgc gcg   547
 67 Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val Tyr Ala Pro Ala Arg Ala
 68 135                 140                 145                 150
 70 ccc ggg gat ccc cag ctg cca gtg atg gtc tgg ttc ccg gga ggc gcc   595
 71 Pro Gly Asp Pro Gln Leu Pro Val Met Val Trp Phe Pro Gly Gly Ala
 72                 155                 160                 165
 74 ttc atc gtg ggc gct gct tct tcg tac gag ggc tct gac ttg gcc gcc   643
 75 Phe Ile Val Gly Ala Ala Ser Ser Tyr Glu Gly Ser Asp Leu Ala Ala
 76             170                 175                 180
 78 cgc gag aaa gtg gtg ctg gtg ttt ctg cag cac agg ctc ggc atc ttc   691
 79 Arg Glu Lys Val Val Leu Val Phe Leu Gln His Arg Leu Gly Ile Phe
 80         185                 190                 195
 82 ggc ttc ctg agc acg gac gac agc cac gcg cgc ggg aac tgg ggg ctg   739
 83 Gly Phe Leu Ser Thr Asp Asp Ser His Ala Arg Gly Asn Trp Gly Leu
 84     200                 205                 210
 86 ctg gac cag atg gcg gct ctg cgc tgg gtg cag gag aac atc gca gcc   787
 87 Leu Asp Gln Met Ala Ala Leu Arg Trp Val Gln Glu Asn Ile Ala Ala
 88 215                 220                 225                 230
 90 ttc ggg gga gac cca gga aat gtg acc ctg ttc ggc cag tcg gcg ggg   835
 91 Phe Gly Gly Asp Pro Gly Asn Val Thr Leu Phe Gly Gln Ser Ala Gly
 92                 235                 240                 245
 94 gcc atg agc atc tca gga ctg atg atg tca ccc cta gcc tcg ggt ctc   883
 95 Ala Met Ser Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu
 96             250                 255                 260
 98 ttc cat cgg gcc att tcc cag agt ggc acc gcg tta ttc aga ctt ttc   931
 99 Phe His Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe
100         265                 270                 275
102 atc act agt aac cca ctg aaa gtg gcc aag aag gtt gcc cac ctg gct   979
103 Ile Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala
104     280                 285                 290
106 gga tgc aac cac aac agc aca cag atc ctg gta aac tgc ctg agg gca  1027
107 Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg Ala
108 295                 300                 305                 310
110 cta tca ggg acc aag gtg atg cgt gtg tcc aac aag atg aga ttc ctc  1075
111 Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg Phe Leu
112                 315                 320                 325
114 caa ctg aac ttc cag aga gac ccg gaa gag att atc tgg tcc atg agc  1123
115 Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu Ile Ile Trp Ser Met Ser
116             330                 335                 340
118 cct gtg gtg gat ggt gtg gtg atc cca gat gac cct ttg gtg ctc ctg  1171
119 Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro Leu Val Leu Leu
120         345                 350                 355
122 acc cag ggg aag gtt tca tct gtg ccc tac ctt cta ggt gtc aac aac  1219
123 Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu Leu Gly Val Asn Asn
124     360                 365                 370
126 ctg gaa ttc aat tgg ctc ttg cct tat atc atg aag ttc ccg cta aac  1267
127 Leu Glu Phe Asn Trp Leu Leu Pro Tyr Ile Met Lys Phe Pro Leu Asn
128 375                 380                 385                 390
130 cgg cag gcg atg aga aag gaa acc atc act aag atg ctc tgg agt acc  1315
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```
131 Arg Gln Ala Met Arg Lys Glu Thr Ile Thr Lys Met Leu Trp Ser Thr
132                 395                 400                 405
134 cgc acc ctg ttg aat atc acc aag gag cag gta cca ctt gtg gtg gag   1363
135 Arg Thr Leu Leu Asn Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu
136             410                 415                 420
138 gag tac ctg gac aat gtc aat gag cat gac tgg aag atg cta cga aac   1411
139 Glu Tyr Leu Asp Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn
140         425                 430                 435
142 cgt atg atg gac ata gtt caa gat gcc act ttc gtg tat gcc aca ctg   1459
143 Arg Met Met Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu
144     440                 445                 450
146 cag act gct cac tac cac cga gat gcc ggc ctc cct gtc tac ctg tat   1507
147 Gln Thr Ala His Tyr His Arg Asp Ala Gly Leu Pro Val Tyr Leu Tyr
148 455                 460                 465                 470
150 gaa ttt gag cac cac gct cgt gga ata atc gtc aaa ccc cgc act gat   1555
151 Glu Phe Glu His His Ala Arg Gly Ile Ile Val Lys Pro Arg Thr Asp
152                 475                 480                 485
154 ggg gca gac cat ggg gat gag atg tac ttc ctc ttt ggg ggc ccc ttc   1603
155 Gly Ala Asp His Gly Asp Glu Met Tyr Phe Leu Phe Gly Gly Pro Phe
156             490                 495                 500
158 gcc aca ggc ctt tcc atg ggt aag gag aag gca ctt agc ctc cag atg   1651
159 Ala Thr Gly Leu Ser Met Gly Lys Glu Lys Ala Leu Ser Leu Gln Met
160         505                 510                 515
162 atg aaa tac tgg gcc aac ttt gcc cgc aca gga aac ccc aat gat ggg   1699
163 Met Lys Tyr Trp Ala Asn Phe Ala Arg Thr Gly Asn Pro Asn Asp Gly
164     520                 525                 530
166 aat ctg ccc tgc tgg cca cgc tac aac aag gat gaa aag tac ctg cag   1747
167 Asn Leu Pro Cys Trp Pro Arg Tyr Asn Lys Asp Glu Lys Tyr Leu Gln
168 535                 540                 545                 550
170 ctg gat ttt acc aca aga gtg ggc atg aag ctc aag gag aag aag atg   1795
171 Leu Asp Phe Thr Thr Arg Val Gly Met Lys Leu Lys Glu Lys Lys Met
172                 555                 560                 565
174 gct ttt tgg atg agt ctg tac cag tct caa aga cct gag aag cag agg   1843
175 Ala Phe Trp Met Ser Leu Tyr Gln Ser Gln Arg Pro Glu Lys Gln Arg
176             570                 575                 580
178 caa ttc taagggtggc tatgcaggaa ggagccaaag aggggtttgc ccccaccatc    1899
179 Gln Phe
182 caggccctgg ggagactagc catggacata cctggggaca agagttctac ccaagggcga 1959
183 attcgtttaa acctgcagga ctag                                       1983
185 <210> SEQ ID NO: 2
186 <211> LENGTH: 584
187 <212> TYPE: PRT
188 <213> ORGANISM: Homo sapiens
190 <400> SEQUENCE: 2
191 Met Pro Ser Thr Val Leu Pro Ser Thr Val Leu Pro Ser Leu Leu Pro
192  1               5                  10                  15
193 Thr Ala Gly Ala Gly Trp Ser Met Arg Trp Ile Leu Cys Trp Ser Leu
194             20                  25                  30
195 Thr Leu Cys Leu Met Ala Gln Thr Ala Leu Gly Ala Leu His Thr Lys
```

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```
196         35                  40                  45
197 Arg Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
198     50                  55                  60
199 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe Ser
200 65                  70                  75                  80
201 Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu
202                 85                  90                  95
203 Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro Gly Cys Leu
204             100                 105                 110
205 Gln Glu Ser Trp Gly Gln Leu Ala Ser Met Tyr Val Ser Thr Arg Glu
206         115                 120                 125
207 Arg Tyr Lys Trp Leu Arg Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val
208     130                 135                 140
209 Tyr Ala Pro Ala Arg Ala Pro Gly Asp Pro Gln Leu Pro Val Met Val
210 145                 150                 155                 160
211 Trp Phe Pro Gly Gly Ala Phe Ile Val Gly Ala Ala Ser Ser Tyr Glu
212                 165                 170                 175
213 Gly Ser Asp Leu Ala Ala Arg Glu Lys Val Val Leu Val Phe Leu Gln
214             180                 185                 190
215 His Arg Leu Gly Ile Phe Gly Phe Leu Ser Thr Asp Asp Ser His Ala
216         195                 200                 205
217 Arg Gly Asn Trp Gly Leu Leu Asp Gln Met Ala Ala Leu Arg Trp Val
218     210                 215                 220
219 Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp Pro Gly Asn Val Thr Leu
220 225                 230                 235                 240
221 Phe Gly Gln Ser Ala Gly Ala Met Ser Ile Ser Gly Leu Met Met Ser
222                 245                 250                 255
223 Pro Leu Ala Ser Gly Leu Phe His Arg Ala Ile Ser Gln Ser Gly Thr
224             260                 265                 270
225 Ala Leu Phe Arg Leu Phe Ile Thr Ser Asn Pro Leu Lys Val Ala Lys
226         275                 280                 285
227 Lys Val Ala His Leu Ala Gly Cys Asn His Asn Ser Thr Gln Ile Leu
228     290                 295                 300
229 Val Asn Cys Leu Arg Ala Leu Ser Gly Thr Lys Val Met Arg Val Ser
230 305                 310                 315                 320
231 Asn Lys Met Arg Phe Leu Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu
232                 325                 330                 335
233 Ile Ile Trp Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp
234             340                 345                 350
235 Asp Pro Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr
236         355                 360                 365
237 Leu Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Ile
238     370                 375                 380
239 Met Lys Phe Pro Leu Asn Arg Gln Ala Met Arg Lys Glu Thr Ile Thr
240 385                 390                 395                 400
241 Lys Met Leu Trp Ser Thr Arg Thr Leu Leu Asn Ile Thr Lys Glu Gln
242                 405                 410                 415
243 Val Pro Leu Val Val Glu Glu Tyr Leu Asp Asn Val Asn Glu His Asp
244             420                 425                 430
```

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Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\12102001\I001227.raw

```
245 Trp Lys Met Leu Arg Asn Arg Met Met Asp Ile Val Gln Asp Ala Thr
246         435                 440                 445
247 Phe Val Tyr Ala Thr Leu Gln Thr Ala His Tyr His Arg Asp Ala Gly
248     450                 455                 460
249 Leu Pro Val Tyr Leu Tyr Glu Phe Glu His His Ala Arg Gly Ile Ile
250 465                 470                 475                 480
251 Val Lys Pro Arg Thr Asp Gly Ala Asp His Gly Asp Glu Met Tyr Phe
252                 485                 490                 495
253 Leu Phe Gly Gly Pro Phe Ala Thr Gly Leu Ser Met Gly Lys Glu Lys
254             500                 505                 510
255 Ala Leu Ser Leu Gln Met Met Lys Tyr Trp Ala Asn Phe Ala Arg Thr
256         515                 520                 525
257 Gly Asn Pro Asn Asp Gly Asn Leu Pro Cys Trp Pro Arg Tyr Asn Lys
258     530                 535                 540
259 Asp Glu Lys Tyr Leu Gln Leu Asp Phe Thr Thr Arg Val Gly Met Lys
260 545                 550                 555                 560
261 Leu Lys Glu Lys Lys Met Ala Phe Trp Met Ser Leu Tyr Gln Ser Gln
262                 565                 570                 575
263 Arg Pro Glu Lys Gln Arg Gln Phe
264             580
267 <210> SEQ ID NO: 3
268 <211> LENGTH: 1752
269 <212> TYPE: DNA
270 <213> ORGANISM: Homo sapiens
272 <220> FEATURE:
273 <221> NAME/KEY: CDS
274 <222> LOCATION: (1)...(1752)
276 <400> SEQUENCE: 3
277 atg cca tcc aca gtg ttg cca tcc aca gtg ttg cca tca ctc ctg ccc   48
278 Met Pro Ser Thr Val Leu Pro Ser Thr Val Leu Pro Ser Leu Leu Pro
279  1               5                  10                  15
281 aca gca gga gct ggc tgg agc atg agg tgg att ctg tgc tgg agc ctc   96
282 Thr Ala Gly Ala Gly Trp Ser Met Arg Trp Ile Leu Cys Trp Ser Leu
283             20                  25                  30
285 acc ctc tgc ctg atg gcg cag acg gcc ttg ggt gcc ttg cac acc aag  144
286 Thr Leu Cys Leu Met Ala Gln Thr Ala Leu Gly Ala Leu His Thr Lys
287         35                  40                  45
289 agg cct caa gtg gtc acc aaa tat gga acc ctg caa gga aaa cag atg  192
290 Arg Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
291     50                  55                  60
293 cat gtg ggg aag aca ccc atc caa gtc ttt tta gga gtc ccc ttc tcc  240
294 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe Ser
295  65                  70                  75                  80
297 aga cct cct cta ggt atc ctc agg ttt gca cct cca gaa ccc ccg gag  288
298 Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu
299                 85                  90                  95
301 ccc tgg aaa gga atc aga gat gct acc acc tac ccg cct ggg tgc ctg  336
302 Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro Gly Cys Leu
303             100                 105                 110
```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/001,227**

DATE: 12/10/2001
TIME: 15:00:39

Input Set : **A:\Seqlist.txt**
Output Set: **N:\CRF3\12102001\I001227.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:494 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5